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Insights into Sphagnum Peat Moss Carbon and Nitrogen Dynamics from CO₂ Flux Analysis and Modeling to Microbiome Analysis

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Sphagnum mosses are foundation species for many peatland ecosystems. With rapid rates of climate change occurring in high latitudes, vast reservoirs of carbon accumulated over millennia in peatland ecosystems are potentially vulnerable to rising temperature and changing precipitation. We explored the carbon and nitrogen cycling responses of *Sphagnum* to warming and CO₂ enrichment as part of the Spruce and Peatland Responses Under Changing Environments (SPRUCE) project in an ombrotrophic spruce bog in the Marcell Experimental Forest in northern Minnesota. Intact plots in the bog are being exposed to a range of warming levels from ambient to ambient +9 °C in combination with ambient or elevated (900 ppm) CO₂ within 12-m diameter, open-top enclosures. Peat moss community analysis shows that the SPRUCE site is dominated by *Sphagnum angustifolium*, *S. fallax* (together comprising 68% cover), and *S. magellanicum* (21% cover). Using clear-topped automatic CO₂ chambers, we investigate the seasonal drivers of *Sphagnum* gross primary production (GPP)—the entry point of carbon into wetland ecosystems. Our CO₂ flux analysis and partitioning show that *Sphagnum* GPP peaked in late summer, well after the peak in photosynthetically active radiation. Wavelet analysis showed that water table height was the key driver of weekly variation in *Sphagnum* GPP in the early summer and that temperature was the primary driver of GPP in the late summer and autumn. We used this information to augment a process-based photosynthetic model that is currently being used by the SPRUCE team. Based on an average *Sphagnum* C:N ratio of 44.3, less than 10% of the N needed to support the observed *Sphagnum* production was accounted for in deposition. Therefore, we explored the impact of SPRUCE imposed experimental warming on the microbial and nitrogen-fixing (diazotroph) community associated with *Sphagnum*. To quantify changes in abundance, diversity, and community composition of *Sphagnum* microbiomes in response to warming, we performed qPCR and Illumina sequencing of SSU rRNA and nitrogenase (*nifH*) genes. Microbial diversity decreased with warming (p<0.05), and diazotrophs shifted from diverse communities to domination by *Nostocaceae* (from 25% in unheated samples to 99% in warmed samples), suggesting that warming influences diversity. Furthermore, temperature increase was negatively correlated with N₂ fixation showing that warming in our system resulted in decreased N₂ fixation. Thus, experimental warming may alter the community structure and function of peat moss microbiomes.